

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Cropdesign NV
- (B) STREET: Technologiepark 3
- (C) CITY: Zwijnaarde
- (D) STATE: none
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): 9052

(ii) TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

(iii) NUMBER OF SEQUENCES: 33

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 86..712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCACGAGGA GAACCACAAA CACGCACACA TAACGAGTGA TTTTAGAGAG AGATAGAGAT
60

CTGGAAGGTG ACGTCGTAGG AGATT ATG GCG GCG GTT AGG AGA AGA GAA CGA
112

Met Ala Ala Val Arg Arg Arg Glu Arg
1 5

GAT GTG GTT GAA GAG AAT GGA GTT ACG ACG ACG ACG GTG AAA CGA AGG
160
Asp Val Val Glu Glu Asn Gly Val Thr Thr Thr Thr Val Lys Arg Arg
10 15 20 25

AAG ATG GAG GAG GAA GTG GAT TTA GTG GAA TCT AGG ATA ATT CTG TCT
208
Lys Met Glu Glu Glu Val Asp Leu Val Glu Ser Arg Ile Ile Leu Ser
30 35 40

ATAAGTTTAT
932

1. Introduction

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
 7. *Chlorophyll g* (Chl *g*)
 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
 11. *Chlorophyll k* (Chl *k*)
 12. *Chlorophyll l* (Chl *l*)
 13. *Chlorophyll m* (Chl *m*)
 14. *Chlorophyll n* (Chl *n*)
 15. *Chlorophyll o* (Chl *o*)
 16. *Chlorophyll p* (Chl *p*)
 17. *Chlorophyll q* (Chl *q*)
 18. *Chlorophyll r* (Chl *r*)
 19. *Chlorophyll s* (Chl *s*)
 20. *Chlorophyll t* (Chl *t*)
 21. *Chlorophyll u* (Chl *u*)
 22. *Chlorophyll v* (Chl *v*)
 23. *Chlorophyll w* (Chl *w*)
 24. *Chlorophyll x* (Chl *x*)
 25. *Chlorophyll y* (Chl *y*)
 26. *Chlorophyll z* (Chl *z*)
 27. *Chlorophyll aa* (Chl *aa*)
 28. *Chlorophyll ab* (Chl *ab*)
 29. *Chlorophyll ac* (Chl *ac*)
 30. *Chlorophyll ad* (Chl *ad*)
 31. *Chlorophyll ae* (Chl *ae*)
 32. *Chlorophyll af* (Chl *af*)
 33. *Chlorophyll ag* (Chl *ag*)
 34. *Chlorophyll ah* (Chl *ah*)
 35. *Chlorophyll ai* (Chl *ai*)
 36. *Chlorophyll aj* (Chl *aj*)
 37. *Chlorophyll ak* (Chl *ak*)
 38. *Chlorophyll al* (Chl *al*)
 39. *Chlorophyll am* (Chl *am*)
 40. *Chlorophyll an* (Chl *an*)
 41. *Chlorophyll ao* (Chl *ao*)
 42. *Chlorophyll ap* (Chl *ap*)
 43. *Chlorophyll aq* (Chl *aq*)
 44. *Chlorophyll ar* (Chl *ar*)
 45. *Chlorophyll as* (Chl *as*)
 46. *Chlorophyll at* (Chl *at*)
 47. *Chlorophyll au* (Chl *au*)
 48. *Chlorophyll av* (Chl *av*)
 49. *Chlorophyll aw* (Chl *aw*)
 50. *Chlorophyll ax* (Chl *ax*)
 51. *Chlorophyll ay* (Chl *ay*)
 52. *Chlorophyll az* (Chl *az*)
 53. *Chlorophyll aza* (Chl *aza*)
 54. *Chlorophyll abz* (Chl *abz*)
 55. *Chlorophyll acz* (Chl *acz*)
 56. *Chlorophyll adz* (Chl *adz*)
 57. *Chlorophyll aez* (Chl *aez*)
 58. *Chlorophyll afz* (Chl *afz*)
 59. *Chlorophyll agz* (Chl *agz*)
 60. *Chlorophyll ahz* (Chl *ahz*)
 61. *Chlorophyll aiz* (Chl *aiz*)
 62. *Chlorophyll ajz* (Chl *ajz*)
 63. *Chlorophyll akz* (Chl *akz*)
 64. *Chlorophyll alz* (Chl *alz*)
 65. *Chlorophyll amz* (Chl *amz*)
 66. *Chlorophyll anz* (Chl *anz*)
 67. *Chlorophyll aoz* (Chl *aoz*)
 68. *Chlorophyll apz* (Chl *apz*)
 69. *Chlorophyll aqz* (Chl *aqz*)
 70. *Chlorophyll arz* (Chl *arz*)
 71. *Chlorophyll asz* (Chl *asz*)
 72. *Chlorophyll atz* (Chl *atz*)
 73. *Chlorophyll auz* (Chl *auz*)
 74. *Chlorophyll avz* (Chl *avz*)
 75. *Chlorophyll awz* (Chl *awz*)
 76. *Chlorophyll axz* (Chl *axz*)
 77. *Chlorophyll ayz* (Chl *ayz*)
 78. *Chlorophyll ayz* (Chl *ayz*)
 79. *Chlorophyll azz* (Chl *azz*)
 80. *Chlorophyll azaa* (Chl *aza*)
 81. *Chlorophyll abz* (Chl *abz*)
 82. *Chlorophyll acz* (Chl *acz*)
 83. *Chlorophyll adz* (Chl *adz*)
 84. *Chlorophyll aez* (Chl *aez*)
 85. *Chlorophyll afz* (Chl *afz*)
 86. *Chlorophyll agz* (Chl *agz*)
 87. *Chlorophyll ahz* (Chl *ahz*)
 88. *Chlorophyll aiz* (Chl *aiz*)
 89. *Chlorophyll ajz* (Chl *ajz*)
 90. *Chlorophyll akz* (Chl *akz*)
 91. *Chlorophyll alz* (Chl *alz*)
 92. *Chlorophyll amz* (Chl *amz*)
 93. *Chlorophyll anz* (Chl *anz*)
 94. *Chlorophyll aoz* (Chl *aoz*)
 95. *Chlorophyll apz* (Chl *apz*)
 96. *Chlorophyll aqz* (Chl *aqz*)
 97. *Chlorophyll arz* (Chl *arz*)
 98. *Chlorophyll asz* (Chl *asz*)
 99. *Chlorophyll atz* (Chl *atz*)
 100. *Chlorophyll auz* (Chl *auz*)
 101. *Chlorophyll avz* (Chl *avz*)
 102. *Chlorophyll awz* (Chl *awz*)
 103. *Chlorophyll axz* (Chl *axz*)
 104. *Chlorophyll ayz* (Chl *ayz*)
 105. *Chlorophyll ayz* (Chl *ayz*)
 106. *Chlorophyll ayz* (Chl *ayz*)
 107. *Chlorophyll ayz* (Chl *ayz*)
 108. *Chlorophyll ayz* (Chl *ayz*)
 109. *Chlorophyll ayz* (Chl *ayz*)
 110. *Chlorophyll ayz* (Chl *ayz*)
 111. *Chlorophyll ayz* (Chl *ayz*)
 112. *Chlorophyll ayz* (Chl *ayz*)
 113. *Chlorophyll ayz* (Chl *ayz*)
 114. *Chlorophyll ayz* (Chl *ayz*)
 115. *Chlorophyll ayz* (Chl *ayz*)
 116. *Chlorophyll ayz* (Chl *ayz*)
 117. *Chlorophyll ayz* (Chl *ayz*)
 118. *Chlorophyll ayz* (Chl *ayz*)
 119. *Chlorophyll ayz* (Chl *ayz*)
 120. *Chlorophyll ayz* (Chl *ayz*)
 121. *Chlorophyll ayz* (Chl *ayz*)
 122. *Chlorophyll ayz* (Chl *ayz*)
 123. *Chlorophyll ayz* (Chl *ayz*)
 124. *Chlorophyll ayz* (Chl *ayz*)
 125. *Chlorophyll ayz* (Chl *ayz*)
 126. *Chlorophyll ayz* (Chl *ayz*)
 127. *Chlorophyll ayz* (Chl *ayz*)
 128. *Chlorophyll ayz* (Chl *ayz*)
 129. *Chlorophyll ayz* (Chl *ayz*)
 130. *Chlorophyll ayz* (Chl *ayz*)
 131. *Chlorophyll ayz* (Chl *ayz*)
 132. *Chlorophyll ayz* (Chl *ayz*

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Ala Val Arg Arg Arg Glu Arg Asp Val Val Glu Glu Asn Gly
 1 5 10 15
 Val Thr Thr Thr Thr Val Lys Arg Arg Lys Met Glu Glu Glu Val Asp
 20 25 30
 Leu Val Glu Ser Arg Ile Ile Leu Ser Pro Cys Val Gln Ala Thr Asn
 35 40 45
 Arg Gly Gly Ile Val Ala Arg Asn Ser Ala Gly Ala Ser Glu Thr Ser
 50 55 60
 Val Val Ile Val Arg Arg Arg Asp Ser Pro Pro Val Glu Glu Gln Cys
 65 70 75 80
 Gln Ile Glu Glu Glu Asp Ser Ser Val Ser Cys Cys Ser Thr Ser Glu
 85 90 95
 Glu Lys Ser Lys Arg Arg Ile Glu Phe Val Asp Leu Glu Glu Asn Asn
 100 105 110
 Gly Asp Asp Arg Glu Thr Glu Thr Ser Trp Ile Tyr Asp Asp Leu Asn
 115 120 125
 Lys Ser Glu Glu Ser Met Asn Met Asp Ser Ser Ser Val Ala Val Glu
 130 135 140
 Asp Val Glu Ser Arg Arg Arg Leu Arg Lys Ser Leu His Glu Thr Val
 145 150 155 160
 Lys Glu Ala Glu Leu Glu Asp Phe Phe Gln Val Ala Glu Lys Asp Leu
 165 170 175
 Arg Asn Lys Leu Leu Glu Cys Ser Met Lys Tyr Asn Phe Asp Phe Glu
 180 185 190
 Lys Asp Glu Pro Leu Gly Gly Gly Arg Tyr Glu Trp Val Lys Leu Asn
 195 200 205
 Pro

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(A) NAME/KEY: CDS
(B) LOCATION: 11..658

GGC	ACG	GAG	AAA	TCA	AAG	ATA	ACT	GGC	GAT	ATC	AGC	GTC	ATG	GAA	GTC
49															
			Lys	Ser	Lys	Ile	Thr	Gly	Asp	Ile	Ser	Val	Met	Glu	Val
			210					215					220		
TCT	AAA	GCA	ACA	GCT	CCA	AGT	CCA	GGT	GTT	CGA	ACC	AGA	GCC	GCT	AAA
97															
Ser	Lys	Ala	Thr	Ala	Pro	Ser	Pro	Gly	Val	Arg	Thr	Arg	Ala	Ala	Lys
		225					230					235			
ACC	CTA	GCC	TTG	AAG	CGG	CTT	AAT	TCC	TCC	GCC	GCT	GAT	TCA	GCT	CTA
145															
Thr	Leu	Ala	Leu	Lys	Arg	Leu	Asn	Ser	Ser	Ala	Ala	Asp	Ser	Ala	Leu
	240					245					250				
CCT	AAC	GAC	TCT	TCT	TGC	TAT	CTT	CAG	CTC	CGT	AGC	CGC	CGT	CTC	GAG
193															
Pro	Asn	Asp	Ser	Ser	Cys	Tyr	Leu	Gln	Leu	Arg	Ser	Arg	Arg	Leu	Glu
255					260					265					270
AAA	CCC	TCT	TCG	CTG	ATT	GAA	CCG	AAA	CAG	CCG	CCG	AGA	GTT	CAC	AGA
241															
Lys	Pro	Ser	Ser	Leu	Ile	Glu	Pro	Lys	Gln	Pro	Pro	Arg	Val	His	Arg
				275					280					285	
TCG	GGA	ATT	AAA	GAG	TCT	GGT	TCC	AGG	TCT	CGC	GTT	GAC	TCG	GTT	AAC
289															
Ser	Gly	Ile	Lys	Glu	Ser	Gly	Ser	Arg	Ser	Arg	Val	Asp	Ser	Val	Asn
			290					295					300		
TCG	GTT	CCT	GTA	GCT	CAG	AGC	TCT	AAT	GAA	GAT	GAA	TGT	TTT	GAC	AAT
337															
Ser	Val	Pro	Val	Ala	Gln	Ser	Ser	Asn	Glu	Asp	Glu	Cys	Phe	Asp	Asn
		305					310					315			
TTC	GTG	AGT	GTC	CAA	GTT	TCT	TGT	GGT	GAA	AAC	AGT	CTC	GGT	TTT	GAA
385															
Phe	Val	Ser	Val	Gln	Val	Ser	Cys	Gly	Glu	Asn	Ser	Leu	Gly	Phe	Glu
	320					325				330					
TCA	AGA	CAC	AGC	ACA	AGG	GAG	AGC	ACG	CCT	TGT	AAC	TTT	GTT	GAG	GAT
433															
Ser	Arg	His	Ser	Thr	Arg	Glu	Ser	Thr	Pro	Cys	Asn	Phe	Val	Glu	Asp
335					340					345					350
ATG	GAG	ATC	ATG	GTT	ACA	CCA	GGG	TCT	AGC	ACG	AGG	TCG	ATG	TGC	AGA
481															
Met	Glu	Ile	Met	Val	Thr	Pro	Gly	Ser	Ser	Thr	Arg	Ser	Met	Cys	Arg
				355					360					365	
GCA	ACC	AAA	GAG	TAC	ACA	AGG	GAA	CAA	GAT	AAC	GTG	ATC	CCG	ACC	ACT
529															
Ala	Thr	Lys	Glu	Tyr	Thr	Arg	Glu	Gln	Asp	Asn	Val	Ile	Pro	Thr	Thr
			370					375					380		
AGT	GAA	ATG	GAG	GAG	TTC	TTT	GCA	TAT	GCA	GAG	CAG	CAG	CAA	CAG	AGG
577				</											

CTA TTC ATG GAG AAG TAC AAC TTC GAC ATT GTG AAT GAT ATC CCC CTC
625

Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu
400 405 410

AGC GGA CGT TAC GAA TGG GTG CAA GTC AAA CCA TGAAGTTCAA AAGGAAACAG
678

Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
415 420 425

CTCCAAAAGA CATGGTGTGA AGTTAGAGAA TGTGATGGAG TTAACAGACT AACCAAACAT
738

CAGAAATCGT GTAATCTTAA GTAATAATGT GGTAGAGAA CAAGTTTGAG AGTAGCTTAG
798

GGACCTTAAA ACCTCACACC ATTTGTAATA CTAATCTTCT TCAGATGCTT AGTGAAATTT
858

TCTCATCTGT TTCTTTC
875

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Lys Ser Lys Ile Thr Gly Asp Ile Ser Val Met Glu Val Ser Lys Ala
1 5 10 15

Thr Ala Pro Ser Pro Gly Val Arg Thr Arg Ala Ala Lys Thr Leu Ala
20 25 30

Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp Ser Ala Leu Pro Asn Asp
35 40 45

Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg Arg Leu Glu Lys Pro Ser
50 55 60

Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg Val His Arg Ser Gly Ile
65 70 75 80

Lys Glu Ser Gly Ser Arg Ser Arg Val Asp Ser Val Asn Ser Val Pro
85 90 95

Val Ala Gln Ser Ser Asn Glu Asp Glu Cys Phe Asp Asn Phe Val Ser
100 105 110

Val Gln Val Ser Cys Gly Glu Asn Ser Leu Gly Phe Glu Ser Arg His
115 120 125

Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp Met Glu Ile
130 135 140

Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg Ala Thr Lys
145 150 155 160

Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr Ser Glu Met
165 170 175

000130"5644560

Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln Gln Gln Arg Leu Phe Met
 180 185 190

Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu Ser Gly Arg
 195 200 205

Tyr Glu Trp Val Gln Val Lys Pro
 210 215

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 92..763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAACCACTCT TCAAATCAAA CACTTTCTTA CATAAGATTC CTCTGTTTTT CTGTGTGCTT
 60

CTTCAAATTC TTCCCCTGTT TTTCAACTTC A ATG GGG AAG TAC ATG AAG AAA
 112

Met Gly Lys Tyr Met Lys Lys
 220

CTC AAA TCC AAA TCA GAA TCT CCT TCA CCC AAT TCA ACA CCA ACA CCA
 160

Leu Lys Ser Lys Ser Glu Ser Pro Ser Pro Asn Ser Thr Pro Thr Pro
 225 230 235

TCA CCA TCA CCA TCA CCA ACA CCA ATC ACC ACC AAT TCA CCA CCA CCA
 208

Ser Pro Ser Pro Ser Pro Thr Pro Ile Thr Thr Asn Ser Pro Pro Pro
 240 245 250 255

ACA ACA CCC AAT TCC TCT GAT GGT GTT CGA ACT CGT GCT AGA ACC CTA
 256

Thr Thr Pro Asn Ser Ser Asp Gly Val Arg Thr Arg Ala Arg Thr Leu
 260 265 270

GCT TTG GAG AAT TCC AAC AAT CAG AAT CAG AAT CTT TCT GTT TCT TCT
 304

Ala Leu Glu Asn Ser Asn Asn Gln Asn Gln Asn Leu Ser Val Ser Ser
 275 280 285

GAT TCT TAC CTT CAG CTG AGG AAC CGT CGC CTT AAG AGA CCC CTA ATT
 352

Asp Ser Tyr Leu Gln Leu Arg Asn Arg Arg Leu Lys Arg Pro Leu Ile
 290 295 300

AGG CAA CAT TCC GCT AAG AGG AAT AAG GGG CAT GAT GGA AAC CCT AAA
 400

Arg Gln His Ser Ala Lys Arg Asn Lys Gly His Asp Gly Asn Pro Lys
 305 310 315
 TCC CCA ATT GGG GAT TCA ATT GCT GAA GAG AAA ACT GTT CAG AAG AGT
 448
 Ser Pro Ile Gly Asp Ser Ile Ala Glu Glu Lys Thr Val Gln Lys Ser
 320 325 330 335
 CCT GAG CCT GAA AAT GCT GAA TTC AAG GAG AAT GCT GAG GAT ACT GAG
 496
 Pro Glu Pro Glu Asn Ala Glu Phe Lys Glu Asn Ala Glu Asp Thr Glu
 340 345 350
 AGA AGC GCT AGG GAA ACT ACA CCC GTC CAT TTG ATA ATG CGA GCA GAC
 544
 Arg Ser Ala Arg Glu Thr Thr Pro Val His Leu Ile Met Arg Ala Asp
 355 360 365
 GTT CTC AGG CCT CCT AGG CCA ATT ACC AGG CGT ACT TTT CCA ACT GAA
 592
 Val Leu Arg Pro Pro Arg Pro Ile Thr Arg Arg Thr Phe Pro Thr Glu
 370 375 380
 GCT AAT CCC AAA ACG GAG CAG CCA ACT ATC CCA ATT TCA CGC GAA TTT
 640
 Ala Asn Pro Lys Thr Glu Gln Pro Thr Ile Pro Ile Ser Arg Glu Phe
 385 390 395
 GAG GAA TTC TGT GCT AAA CAT GAA GCC GAG CAG CAA AGG GAG TTC ATG
 688
 Glu Glu Phe Cys Ala Lys His Glu Ala Glu Gln Gln Arg Glu Phe Met
 400 405 410 415
 GAG AAG TAC AAC TTT GAT CCT GTG ACA GAG CAG CCA CTC CCA GGG CGT
 736
 Glu Lys Tyr Asn Phe Asp Pro Val Thr Glu Gln Pro Leu Pro Gly Arg
 420 425 430
 TAC GAA TGG GAA AAA GTG TCG CCC TAG AAGGCAGGCT AGTATTAAGT
 783
 Tyr Glu Trp Glu Lys Val Ser Pro *
 435 440
 GTTCCATCAA TACATCTTTA AAGTAGCAGC AGGGTTAGAA TTTGTTGAAA AGGGTGGTGG
 843
 TGCTATTTCC ATTTTCCATC ACTTTCTATT TACTTGTAAG GAAAGTAGGA CTTTCAACAT
 903
 ATGTAGACTA ATGATCTGTA ACTTTACAGA GGTGTTGATT ACACAACAAT ACAAAGTCCT
 963
 TTGTCTAGCA GATCATTAAG GAAGGGTTTG AGGGAATAAG GGTCTCTAGT TGTAGGGTTT
 1023
 AGGGTATAAA ATCAAAGTAG GGTATGTAAG AGAGGTTTTA CAAGAATTTT CTTTTGTTCT
 1083
 TGTGTTTTTAC TCTTGTTTTG TCTATACTTG TACTCATGGA ACTTCAACAA ACTCTTAAGA
 1143
 AATAAGAAG CAGATCTCCC TCAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 1193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Gly Lys Tyr Met Lys Lys Leu Lys Ser Lys Ser Glu Ser Pro Ser
1 5 10 15

Pro Asn Ser Thr Pro Thr Pro Ser Pro Ser Pro Ser Pro Thr Pro Ile
20 25 30

Thr Thr Asn Ser Pro Pro Pro Thr Thr Pro Asn Ser Ser Asp Gly Val
35 40 45

Arg Thr Arg Ala Arg Thr Leu Ala Leu Glu Asn Ser Asn Asn Gln Asn
50 55 60

Gln Asn Leu Ser Val Ser Ser Asp Ser Tyr Leu Gln Leu Arg Asn Arg
65 70 75 80

Arg Leu Lys Arg Pro Leu Ile Arg Gln His Ser Ala Lys Arg Asn Lys
85 90 95

Gly His Asp Gly Asn Pro Lys Ser Pro Ile Gly Asp Ser Ile Ala Glu
100 105 110

Glu Lys Thr Val Gln Lys Ser Pro Glu Pro Glu Asn Ala Glu Phe Lys
115 120 125

Glu Asn Ala Glu Asp Thr Glu Arg Ser Ala Arg Glu Thr Thr Pro Val
130 135 140

His Leu Ile Met Arg Ala Asp Val Leu Arg Pro Pro Arg Pro Ile Thr
145 150 155 160

Arg Arg Thr Phe Pro Thr Glu Ala Asn Pro Lys Thr Glu Gln Pro Thr
165 170 175

Ile Pro Ile Ser Arg Glu Phe Glu Glu Phe Cys Ala Lys His Glu Ala
180 185 190

Glu Gln Gln Arg Glu Phe Met Glu Lys Tyr Asn Phe Asp Pro Val Thr
195 200 205

Glu Gln Pro Leu Pro Gly Arg Tyr Glu Trp Glu Lys Val Ser Pro *

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "oligonucleotide"
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(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGAGATCTGA ATTCATGGAT CAGTA
25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGAGATCTGA ATTCCTAAGG CATGCC
26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGGAATCCAT GGGCGGCGGT TAGGAGAAG
29

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGCGGATCCC GTCTTCTTCA TGGATTC
27

CGAGATCTGA ATTCCTAAGG CATGCC

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 29 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCGAATCCA TGGAAGTCTC TAAAGCAAC
29
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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 30 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCGGATCCT TTTGAACTTC ATGGTTTGAC
30
```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CGGCTCGAGG AGAACCACAA ACACGC

26

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CGAAACTAGT TAATTACCTC AAGGAAG
27

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCCCGGGC GATATCAGCG TCATGG
26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCCCGGGT TAGTCTGTTA ACTCC
25

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

003730 "CE" 003730

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

(2) INFORMATION FOR SEQ ID NO: 21:

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"

iii) HYPOTHETICAL: YES
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CGAAACTAGT TAATTACCTC AAGGAAG
27

(2) INFORMATION FOR SEQ ID NO: 22:

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"

iii) HYPOTHETICAL: YES
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GATCCCGGGC GATATCAGCG TCATGG
26

(2) INFORMATION FOR SEQ ID NO: 23:

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

(2) INFORMATION FOR SEQ ID NO: 24:

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCCGCTCGAG ATGGTGAGAA AATATAGAAA AGCTAAAGGA TTTGTAGAAG CTGGAGTTTC
60

GTCAACGTA
69

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGACTAGTTC ACTCTAACTT TACCCATTCTG
30

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(iii) HYPOTHETICAL: YES

TAGGAGCATA TGGCGGCGG
19

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATATCAGCGC CATGGAAGTC
20

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGAGCTGGAT CCTTTTGGAA TTCATGG
27

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(iii) HYPOTHETICAL: YES

TAGGAGCATA TGGCGGCGG
19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ATCATCGAAT TCTTCATGGA TTC
23

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATATCAGCGC CATGGAAGTC
20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGAGCTGGAT CCTTTTGGAA TTCATGG

27

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

VRRRD/EXXVEE

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2023-2024